

3. (amended) The recombinant nucleic acid of claim 1 wherein the 5' region of the plant

*FAE1* gene comprises (5' to 3'):

AAGGCTTACC CTATTAGTTG AAAGTTGAAA CTTTGTTCOC TACTCAATTC CTAGTTGTGT  
AAATGTATGT ATATGTAATG CGTATAAAAC GTAGTACTTA AATGACTAGG ASTGGTTCTT  
GAGACCGATG AGAGATGGGA GCAGAACTAA AGATGATGAC ATAATTAAGA ACSAATTTGA  
AAGGCTCTTA GGTTTGAATC CTATTGAGAA ATGTTTTTGT CAAAGATAGT GGCGATTTTG  
AADCAGAGAA AACATTTTAA AAATCAGTAT CCGGTTACGT TCATGCAAAAT AGAAAGTGGT  
CTAGGATCTG ATTGTAAATT TAGACTTAAA GAGTCTCTTA ACATTCAATC CTGGCTGTGT  
ACAAAACCTAC AAATAATATA TTTTAGACTA TTTGGGCTTA ACTAAACTTC CACTCATTAT  
TTACTGAGGT TAGAGAATAG ACTTGCGAAT AAACACATTC CCGAGAAATA CTCATGATCC  
CATAATTAGT CAGAGGGTAT GCCAATCAGA TCTAAGAAAC CACATTCCCT CAAATTTTAA  
TGCACATSTA ATCATAAGTTT AGCACAATTC AAAAATAATG TAGTATTAAA GACAGAAATT  
TGTAGACTTT TTTTGGCGT TAAAGGAAGA CTAAGTTTAT ACGTACATTT TATTTTAAGT  
GGAAAACCGA AATTTTCCAT CGAAATATAT GAATTTAGTA TATATATTC TGCAATGTAC  
TATTTTCTA TTTTGGCAAC TTTCAGTGGG CTACTACTTT ATTACAATGT GTATGGATGC  
ATGAGTTTGA GTATACACAT GTCTAAATGC ATGCTTTTGA AAACGTAACG GACCACAAAA  
GAGGATCCAT GCAAATACAT CTCATAGCTT CCTCCATTAT TTTCCGACAC AAACAGAGCA  
(SEQ ID NO: 16).

4. (amended) The recombinant nucleic acid of claim 1 wherein the 5' region of the plant

*FAE1* gene comprises (5' to 3'):

CTGACTTC ACCAAAGAAA CAACTCGAGT CGTTATCCAT CTCTCATAA  
CCATCGCTCC ACTTTTGGC TTCACCGTTT TCGGTTGGGT TCTCTACATC GCAACCGGGC  
CCAAACCGGT TTACCTCGTT GAGTACTCAT GCTACCTTCC ACCAACGCAT TGTAGATCAA  
GTATCTCCAA GGTGATGGAT ATCTTTTATC AAGTAAGAAA AGCTGATCCT TCTCGGAACG  
GCACGTGCGA TGACTCGTCC TGGCTTGAAT TCTTGAGGAA GATTCAAGAA CGTTCAGSTC  
TAGGCGADGA AACTCAGGG CCGAGGGGGC TGCTTCAGGT CCGTCCCGGG AAGACTTTTG  
CGGCGGCGCG TGAAGAGACG GAGCAAGTTA TCATTGGTGC GTAGAAAAAT CTATTCAAGA  
ACACCAAGGT TAAACCTAAA GATATAGGTA TACTTGTGGT GAACTCAAGC ATGTTTAATC  
CAACTCCATC GCTCTCGGC ATGGTCTTAA ACACCTTCAA GCTCGAAGC AAGTAAAGAA  
GCTTTAAGCT TGGTGGCATG GGTGTASTG CCGGCTTAT AGGCATTGAT CTAGCAAAGG  
ACTTGTGCA TGTCCATAAA AATACGTATG CTCTTGTGGT GAGCAGAGAG AACATCACTT  
ATAACATTTA CGCTGGTGAT AATAGGTCCA TGATGGTTTC AAATTGCTTG TCGGTGTTG  
GTGGGGCGGC TATTTTCTC TCGAACAAAG CTGGAGATCG TAGACGGTCC AAGTACGAGC

TAGTTCACAC GGTTCGAACG CATACCGGAG CTGACGACAA GTCTTTTCTG TGGGTGCAAC  
AAGGAGACGA TSAGAACGGC AAAATCGGAG TGAGTTTGTG CAAGGACATA ACCGATGTTG  
CTGSTCGAAC GGTTAAGAAA AACATAGCAA CGTTGGGTCG GTTGATTCTT CGGTAAAGCG  
AGAAACTTCT TTTTTTCTGT ACCTTCATGG GCAAGAAACT TTTCAAGAT AAAATCAAAC  
ATTACTACGT CCGCGATTTC AAACCTGCTA TTGACCATTT TTGTATACAT CGCGGAGGCA  
GAGCGGTGAT TGATGTGCTA GAGAAGAAAC TAGCCCTAGC ACCGATCGAT GTAGAGGCAT  
CAAGATCAAC GTTACATAGA TTTGGAACA CTTCATCTAG CTCAATATGG TATGAGTTGG  
CATACATAGA AGCAAAAGGA AGGATGAAGA AAGSTAATAA AGTTTGGCAG ATTGCTTTAG  
GGTCAGGCTT TAASTGTAAC AGTGCAGTTT GGGTGGCTCT AAACAATGTC AAAGCTTGA  
CAAATAGTCC TTGGGAACAC TGCATCGACA GATACCGGT CAAAAATTGAT TCTGATTGAG  
GTAAGTCAGA GACTGCTGTC CAAAAAGGTC GGTCTAATA AACGATGTTT GCTCTCTTC  
GTTTCTTTTT ATTTGTTATA ATAATTTGAT GGCTACGATG TTTCTCTTGT TTGTTATGAA  
TAAAGAATGC AATGGTGTTC TAGTATTTGA TTGTTTTACA TGATGTATC TCTTATTTAC  
ATGAAATTTT TAAACGGCTA AAAAAAAAAA CGGAATTCGG (SEQ ID NO: 17).

5. (amended) The recombinant nucleic acid of claim 1 wherein the 5' region of the plant *FAE1* gene comprises (5' to 3'):

CAGCTTAAC CGGTAAAATT GGGCTGTACA  
TATATTTACC ACTGAGTAAA GACATCAGTT AATGATTTGT TCTTACTCAA TTGGGCTAAG  
TGTATTATTA TATGTGTTGT ATATAATAAA GGTAGAACGT AAATTTACTA AGAATGTGTT  
TTTCCAATGT GATTGCTCTT TGGGCTCTTA GGTTTGAATC CTACTCGAGA AGACTAATTT  
TAATTTACTG GCAAAAATAG AAATCAATTT ATAAGTGTTT AAACAAATCG ATGGTATAAC  
TGATTAGTGA TCACTCTTAG GTTTTGATCC AACTCGAGTA TTGAGTATTG AACGCTTTTT  
TTAAATAAAA TCTTGATTTT TAAATTGGTT TTTTGAGTAA AAAAGTTCTT AATATTTCTT  
CTTTGTTTTA ATGGGTTTGT TTTGCATTTT ATAAGCTTAA TTTTCTAAT TTAATATTTT  
ATCTATCATC GTCCGTAAAG TTTTATTTGG CACAACTTG TTTTACTTTT CTACCTTATA  
ATTTGGGAAC TGGTTGAGTC AAAGGCTACC GGACAAATAT GTTTTATATT CTATTTTAAG  
AATTAACACT CATCTCATAA TTAGTCAGAG GCTAGGAGAG TTCAGCCAAT CAATGCTAAC  
AACAAAATTC TCTTAATGAT CTAACGATGC TATTTAATAT TGGGATCAGT ATTCTTAAAT  
AAGAATATAA AACTAATTCA ATAGTTACAG ATAAAACTT ATATAGACTT TTTTATTTGG  
AATATAAAAG TATCAATATA TTATAGACAA TATTTATAAC GTTAAAAATA CAATATTTAT  
ATTTTTTATA TATTTATTTT AAATTGAAAA GCATTACTTC TATCGAAATG AATTTTAGTA  
TATTAATTAA TATTTTTTTA ATGGGACTAC TTTCTATTT TGGCAGCTTT CATCTGACTA  
CTAATTTATT TCAATGTGTA TGCATGCATG AGCATGAGTA ATACCATST CTATATAAAT

GCATGTAAAA CGTAACGGAC CACAAAAGTG GATCCATACA AATACATCTC ATCGCACCCCT  
CTCCGACACA AAACCTGAACA (SEQ ID NO: 18).

7. (amended) The recombinant nucleic acid of claim 6, wherein the transcriptional regulatory region is at least 70% identical when optimally aligned to the 5' region of the plant *FAEI* gene.

8. (amended) The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):

AGA TCTAAGAACA CACATTCCCT CAAATTTTAA TGCACATGTA  
ATCATAGTTT AGCACAATTC AAAAATAATG TAGTATTAAA GACAGAAATT TGTAGACTTT  
TTTTTGGCGT TAAAGGAAGA CTAAGTTTAT ACGTACATTT TATTTTAAAGT GGAAAACCGA  
AATTTTCCAT CGAAATATAT GAATTTAGTA TATATATTTT TSCAATGTAC TATTTTGCTA  
TTTTGGCAAC TTTCAGTGGG CTACTACTTT ATTACAATGT STATGGATGC ATGAGTTTGA  
GTATACACAT GTCTAAATGC ATGCTTTTGA AAACGTAAAG GACCACAAAA GAGGATCCAT  
GCAAATACAT CTCATAGCTT CCTCCATTAT TTTCCGACAC AAACAGAGCA (SEQ ID  
NO: 15).

9. (amended) The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):

AAGGCTTACC CTATTAGTTG AAAGTTGAAA CTTTGTTCCT TACTCAATTC CTAGTTGTGT  
AAATGTATGT ATATGTAATG CSTATAAAAC GTAGTACTTA AATGACTAGG AATGTTCTCT  
GAGACCGATG AGAGATGGGA GCAGAACTAA AGATGATGAC ATAATTAAGA ACGAATTTGA  
AAGGCTCTTA GGTTTGAATC CTATTCGAGA ATGTTTTTGT CAAAGATAGT GGGGATTTTG  
AACCAAAGAA AACATTTAAA AAATCAGTAT CCGGTTACGT TCATGCAAAT AGAAAGTGGT  
CTAGGATCTG ATTGTAAATT TAGACTTAAA GAGTCTCTTA AGATTCAATC CTGGCTGTGT  
ACAAAACCTAC AAATAATATA TTTTAGACTA TTTGGCCTTA ACTAACTTC CACTCATTAT  
TTACTGAGGT TAGAGAATAG ACTTGCGAAT AAACACATTC CCGAGAAATA CTCATGATCC  
CATAATTAGT CAGAGGSTAT GCGAATCAGA TCTAAGAACA CACATTCCCT CAAATTTTAA  
TGCACATGTA ATCATAGTTT AGCACAATTC AAAAATAATG TAGTATTAAA GACAGAAATT  
TGTAGACTTT TTTTTGGCGT TAAAGGAAGA CTAAGTTTAT ACGTACATTT TATTTTAAAGT  
GGAAAACCGA AATTTTCCAT CGAAATATAT GAATTTAGTA TATATATTTT TSCAATGTAC  
TATTTTGCTA TTTTGGCAAC TTTCAGTGGG CTACTACTTT ATTACAATGT STATGGATGC

ATGAGTTTGA GTATACACAT GTCTAAATGC ATGCTTTTGA AAACGTAAAC GACACAAAA  
GAGGATCCAT GCAAATACAT CTCATAGCTT CCTCCATTAT TTCCGACAC AAACAGAGCA  
(SEQ ID NO: 16).

10. (amended) The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):

CTGACTTC ACCAAAGAAA CAACTCGAGT CGTTATCCAT CTCTCATAA  
CCATCGCTCC ACTCTTTGCC TTCACTTTT TGGTTTGGT TCTCTACAT GCAACCGGCG  
CCAAACCGGT TTACCTCGTT GAGTACTCAT GCTACCTTCC ACCAACGCAT TGTAGATCAA  
GTATCTCCAA GGTCATGGAT ATCTTTTATC AAGTAAGAAA AGCTGATCCT TCTCGGAACG  
GCACGTGGCA TGACTCGTGG TGGCTTGAAT TCTTGAGGAA GATTCAAGAA CGTTCAGGTC  
TAGGCGATGA AACTCAGGGG CCGGAGGGGG TGCTTCAGGT CCTCCCGGG AAGACTTTTG  
CGGCGGCGCG TGAAAGAGACG GAGCAAGTTA TCATTGGTGC GCTAGAAAAT CTATTCAAGA  
ACACCAACGT TAACCTTAAA GATATAGGTA TACTTGTGGT GAACTCAAGC ATGTTTAATC  
CAACTCCATC GCTCTCCGCG ATGCTCTGTA ACACTTTCAA GCTCCGAAGC AAGTAAGAA  
GCTTTAACCT TGGTGGCATG GGTGTAAGTG CCGGGGTTAT AGCCATTGAT CTAGCAAAGG  
ACTTGTGCA TGTCATAAAA AATAGTATG CTCTTGTGGT GAGCAGAGAG AACATCACTT  
ATAACATTTA CGCTGGTAT AATAGGTCCA TGATGGTTTC AAATTGCTTG TTGGTGTG  
GTGGGGCGCG TATTTTCTC TCCAACAAGC CTGGAGATCG TAGACGGTCC AAGTACGAGC  
TAGTTCACAC GGTTCGAACG CATACCGGAG CTGACGACAA GTCTTTTCTG TGCTGCAAC  
AAGGAGACGA TGAGAACGGC AAAATCGGAG TGAGTTTGTC CAAGGACATA ACGATGTTG  
CTGGTGAAC GGTAAAGAAA AATATAGCAA CGTTGGGTCC GTTGATTCTT CGTTAAGCG  
AGAACTTCT TTTTTCGTT AACTTCATGG GCAAGAAACT TTTCAAGAT AAAATCAAAC  
ATTACTACGT CCGGATTTT AAACCTGCTA TTGACCATTT TTGTATACAT CCGGAGGCA  
GAGCGTGAT TGATGTGCTA GAGAAGAAC TAGCCCTAGC ACGATCGAT GTAGAGGCAT  
CAAGATCAAC GTTACATAGA TTTGGAAACA CTTCATCTAG CTCAATATGG TATGAGTTGG  
CATACATAGA AGCAAAAGGA AGGATGAAGA AAGSTAATAA AGTTTGGCAG ATTGCTTTAG  
GGTCAGGCTT TAAGTGTAAC AGTGCAGTTT GGGTGGCTCT AAACAATGTC AAAGCTTGA  
CAAATAGTCC TTGGGAACAC TGCATCGACA GATACCGGT CAAAATTGAT TCTGATTCAG  
GTAAGTCAGA GACTCGTGTG CAAAACGGTC GGTCCTAATA AAGGATGTTT GCTCTCTTTC  
GTTTCTTTTT ATTGTGATA ATAATTTGAT GGCTACGATG TTTCTCTTGT TTGTTATGAA  
TAAAGAATGC AATGGTGTTC TAGTATTTGA TTGTTTACA TGATGATC TCTTATTCAC  
ATGAAATTTT TAAACGCTA AAAAAAAAAA CGGAATTCGG (SEQ ID NO: 17).